

IN THE SPECIFICATION:

Please amend the specification, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows:

Page 63, line 1:

Cassette 1- Translation initiation signal and signal peptide

In order to achieve correct translation initiation and secretion from mammalian cells, the following sequence is used (SEQ ID NO 16):

aagcttCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
GTCCACTCC (SEQ ID NO: 38)

This contains a convenient *Hind*III restriction site for cloning into expression vectors (lower case), the consensus translation initiation signal for mammalian cells (ANNATGPu) and the coding sequence for a signal peptide sequence from an immunoglobulin gene.

Page 70, line 6:

The flexible linker, used to join the extracellular domain of B7.1 and the ScFv, was constructed by annealing two homologous oligonucleotides with engineered 5' Sma I and 3' Spe I sites - using oligonucleotides

upper (SEQ ID NO: 6)

5' GGG GGT GGT GGG AGC GGT GGT GGC GGC AGT GGC GGC GGC GGA A 3'

and lower (SEQ ID NO: 16)

5' CTA GTT CCG CCG CCG CCA CTG CCG CCA CCA CCG CTC CCA CCA CCC CC 3'

The linker is cloned into pBluescript (Stratagene) via Sma I and Spe I to produce pLINK. The signal peptide (sp) and extracellular domain of murine B7.1 were amplified by PCR from

pLK444-mB7.1 (supplied by R. Germain NIH, USA) via primers that introduce 5' EcoRI and 3' Sma I sites - primers forward

Page 68, line 18:

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5' C TCG AAT TCC ACC ATG GCT TGC AAT TGT CAG TTG ATG C 3'

reverse (SEQ ID NO: 18)

5' CTC CCC GGG CTT GCT ATC AGG AGG GTC TTC 3'

The B7.1 PCR product was cloned into pLINK via Eco RI and Sma I to form pBS/B7Link.

The V_H and V_L of the 5T4 specific ScFv was amplified via primers -

forward primer (SEQ ID NO: 19)

5' CTC ACT AGT GAG GTC CAG CTT CAG CAG TC 3'

reverse primer (SEQ ID NO: 20)

5' CTC GCG GCC GCT TAC CGT TTG ATT TCC AGC TTG GTG CCT CCA CC 3'

that introduce 5' Spe I and 3' Not I sites from pHEN1-5T4 ScFv. PBS/B7Link was digested with Spe I and Not I and ligated with the ScFv to form OBM 233 consisting of the sequence shown as SEQ ID No. 11: B7 Link ScFv sequence (Figure 5).

Page 71, line 5:

The sequence encoding a translation initiation sequence and the human immunoglobulin kappa light chain signal peptide is synthesized as two complementary single stranded oligonucleotides which when annealed also contain an internal *Xho I* site at the 5' end and in addition leave a *Xba I* compatible 5' overhang and a *Pst I* compatible 3' overhang

ctagactcgagCCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA
GCT ACA GGT GTC CAC TCC GAG GTC CAG ctgca (SEQ ID NO: 21)

and

g CTG GAC CTC GGA GTG GAC ACC TGT AGC TGT TGC TAC CAA GAA GAG GAT
GAT ACA GCT CCA TCC CAT GGTGGctcgagt (SEQ ID NO: 22)

This is then cloned into pBluescript II (Stratagene) restricted with *Xba I* and *Pst I* to create pBSII/Leader.

Page 71, line 21:

The 5T4 ScFv is amplified by PCR from pHEN1 using oligonucleotides which incorporate a *Pst I* site at the 5' end of the product and a *Hind III* at the 3' end

GTC CAG CTG CAG CAG TCT GG (SEQ ID NO: 23)

and

CG TTT GAT TTC AAG CTT GGT GC (SEQ ID NO: 24)

This is then restricted with those enzymes and inserted into pBSII/Leader restricted with the same enzymes, creating pBSII/Leader/ScFv.

Page 72, line 1:

The HIgG 1 constant region is amplified by PCR from the cloned gene using oligonucleotides which incorporate a *Hind III* site at the 5' end and a *Xho I* site at the 3' end

gcgc AAG CTT gaa atc aaa cgg GCC TCC ACC AAG GGC CCA (SEQ ID NO: 25)

and

gcgc ctcgag TCA TTT ACC CGG AGA CAG GG (SEQ ID NO: 26)

This is then restricted with those enzymes and inserted into pBSII/Leader/ScFv restricted with the same enzymes, creating pBSII/Leader/ScFv/HG1. The sequence for this construct is shown in the Figure 4 (SEQ ID No 10).

Page 72, line 29:

This fusion construct is made by amplifying the human IgE1 constant heavy region by PCR cDNA derived from human B-cells RNA by RT and subsequently using oligonucleotides which incorporate a *Hind III* site at the 5' end and a *Xho I* site at the 3' end

gcgc AAG CTT gaa atc aaa cgg GCC TCC ACA CAG AGC CCA (SEQ ID NO: 27)

and

gcgc ctcgag TCA TTT ACC GGG ATT TAC AGA (SEQ ID NO: 28)

This is then restricted with those enzymes and inserted into pBSII/Leader/ScFv restricted with the same enzymes, creating pBSII/Leader/ScFv/HE1.

Page 74, line 1:

Using cDNA derived by RT of RNA isolated from a cell line such the 293 human kidney line (ATCC: CRL1573), the DNA is amplified by PCR using oligonucleotides containing a *Spe I* restriction enzyme site at the N-terminus and a stop codon and a *Not I* site at the C-terminus

GG ACT AGT AAT AGT GAC TCT GAA TGT CCC (SEQ ID NO: 29)

And

ATT AGC GGC CGC TTA GCG CAG TTC CCA CCA CTT C (SEQ ID NO: 30)

The resulting product is digested with those enzymes and ligated to pBS/B7 Link which has been restricted with the same enzymes creating pBS/B7 Link EGF. The B7 Link EGF cassette is then excised with *Eco RI* and *Not I* and inserted into a derivative of pHIT111 (Soneoka *et al*, 1995, Nucl Acid Res 23; 628) which no longer carries the *LacZ* gene.

Page 80, line 29:

For B7-5T4 scFv the primers are as follows:-

Primer 1. B7-Sbf

ATCGCCTGCAGG***CCACC***ATGGCTTGCAATTGTCAG (SEQ ID NO: 31)

Sbf I site = underlined

Kozak sequence = bold and italics with the ATG start codon underlined.

Primer 2. 5T4sc-RI

GCGCGAATTC***TTACCGTTTGATTTC***AGCTTGGT (SEQ ID NO: 32)

Eco RI site = underlined

TAA stop codon = bold and italics

The resultant product is then cloned into pONY 8.1 SM to produce the fusion protein construct shown in Figure 19a.

For L-5T4 scFv the primers are as follows:-

Primer 1. L-Sbf

ATCGCCTGCAGGCCACCA***ATG***GATGGAGCTGTAT (SEQ ID NO: 33)

Sbf I site = underlined

Kozak sequence = bold and italics, with the ATG start codon underlined.

Primer 2. 5T4sc-RI

GCGCGAATTC***TTA***ACCGTTTGATTTCAGCTTGGT (SEQ ID NO: 34)

Eco RI site = underlined

TAA stop codon = bold and italics

The resultant product is then cloned into pONY 8.1 SM to produce the construct shown in Figure 19b.